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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
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iigh quality sequence stop: 412.
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                          with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation
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                                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                Department of Agronomy and Plant Genetics University of Minnesota
                                                                                                                        ESTS
                                                                                                                                                                                                                                                                                                                                              sequence.
AW980848
AW980848.1 GI:8172391
                                                                                                                                                                                                                                                                                                                                                                                                     AW980848 698 bp mRNA EST 02-JUN-2000 EST392001 GVN Medicago truncatula cDNA clone pGVN-58L14, mRNA
                                                           Contact: Carroll P. Vance
                                                                            Unpublished (2000)
                                                                                                                                           Holt, I.E. and Fraser, C.M.
                                                                                                                                                            Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., P, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S.,
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411 Borlaug Hall, 1991 Upper Buford Circle,
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                                                                                                                      from one month old nitrogen-fixing root nodules of Medicago
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                AW684493 564 bp mrNA NF017F01NR1F1000 Nodulated root NF017F01NR 5', mRNA sequence.
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University of Minnesota name:M256682e
TICR sequence name:MTCBR67TK
More information is available at. h
More information for available at. h
AW684493
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Location/Qualifiers
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/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
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/culitivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-58L14"
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gagacacttttgagggccgttgagagctacctcttggcacactccgatgcctacaac
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundat
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Fax: 580 221 7380
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Expressed Sequence Tags from the Samuel Roberts Noble
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Insert Length: 564 Std Error: 0.0
Plate: 017 row: F column: 01
Seq primer: TCACACAGGAAACAGCTATGAC
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a 95 c 125 g 174 t 2 others
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/tissue_type="root"
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/db_xref="taxon:3880"
/clone="NF017F01NR"
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                    gttgaaaacattgaaggaaatggagggcctggaaccattaagaagatcagctttcccgaa 180
 gcctttatccttgatggcgataacctctttccaaaggttgcaccccaagccattagcagt 120
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK 73401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison, M.J., Liu, J., Harris, A.R., Gonzales, M.B. and Ellis, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 1/23/00; Updated to the Database of Expressed Sequence (dbEST) on 04/27/00; More information is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jan 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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1 (bases 1 to 548)
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580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from phosphate starved roots
                                                                                                                                                                                                                                                                              //dev_stage="phosphate starved"
//dev_stage="phosphate starved"
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; At the trifoliate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this 30 day period, they were
fertilized twice weekly with 1/2 Hoaglands solution
containing only 20uM potassium phosphate. RNA was prepared
from the roots. cDNA was prepared from polyA+ enriched
RNA. The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in SOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Jemalong, line
/db_xref="taxon:3880"
/clone="MHRP-24F8"
/clone_lib="rootphos(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="roots"
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/cultivar="Jemalong, line A17"
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Medicago truncatula
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Pred. No. 6.4e-38;
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VandenBosch, K., Hurt, J.,
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290 TACAACTACAGCATAGTTGGTGGTGGTGGACTTCCAGACACAGTGGAGAAGATCTCCTTT 349
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http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA 9AA CTA gt.
Location/Qualifiers
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TIGR sequence name:MTIAK73TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kate@mail.bio.tamu.edu
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packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

100 c 147 g 206 t
                                                                                                              /note-"Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; Call was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts
                                                                                                                                                                                                                                                                                                                 /tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
mellioti ABS7M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                /lab_host="E. coli strain SOLR"
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                                                                                                       2510 Sam Noble Parkway,
Tel: 580 221 7317
Fax: 580 221 7380
                                                                                                                                COntact. .....
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                                                                                                                                     ,G.D. and Paiva,N.L. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula nodulated root library Unpublished (2000)
                                                                                                                                                                                                                              Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Gonzales, R.A., Bell, C.J., Flores, H.R., It, G.D. and Paiva, N.L.
                                                                                                                                                                                                                                                                                                                                                                                   AW686778 643 bp mRNA EST 15-JUN-
NF042G08NR1F1000 Nodulated root Medicago truncatula cDNA
NF042G08NR 5', mRNA sequence.
                                                 Email: nlpaiva@noble.org
Insert Length: 643 Std Error: 0.0
Plate: 042 row: G column: 08
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                           Contact: Paiva NL
                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Medicago.

1 (bases 1 to 643)

1 (bases 1 to 643)
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barrel medic.
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                          1. .643
/organism="Medicago truncatula"
/db_xref="taxon:3880"
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Pred. No. 6.6e-38;
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Query Match
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Texas A&M University
College Station, TX 77843-3258,
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Medicago.
                                                                                    Contact: VandenBosch
Department of Biology
                                                                                                                                     ESTs from roots of Medicago truncatula after Rhizobium Unpublished (1999)
                                                                                                                                                                                    Town, C.D., Bowman, C.L., Fraser, C.M.
                                                                                                                                                                                                                          1 (bases 1 to 661)
VandenBosch, K., Hurt, J.,
                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
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/note="Vector: Lambda Zap; Four-week old Rhizobium 
meliloti-inoculated Medicago truncatula roots, containing 
a mixture of young and old roots and nodules." 
a 102 c 143 g 213 t
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/tissue_type="root"
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Pred. No. 6.7e-38;
0; Mismatches 185;
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pKV1-5L19, mRNA
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sequence.
AW980491
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EST.
                                                                  AW980491
EST391644 GVN
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Seq primer: SKmod (CTA gAA CTA gtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kate@mail.bio.tamu.edu
Texas A&M University:T263236e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells." a 102 c 151 g 219 t
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/dev_stage="24 hours post-ino
meliloti ABS7M"
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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV1-5L19"
/clone_lib="KV1"
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pred. No. 6.8e-38;
0; Mismatches 185
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gagataaagatagtggcaacccctgatggaggatccatcttgaagatcagcaacaagtac
                                                                                                                               ggcctccctttcaagtacgtgaaggacagagttgatgaggtggaccacacaaacttcaaa
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Department of Agronomy and Plant Genetics
University of Minnesota
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More information is available at. . http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
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/dev_stage="effective root nodules harvested one month
/dev_stage="effective root nodules harvested one month
/post incoulation with Sinorhizobium meliloti"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK +/; Site_1: EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI
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/clone_lib="GVN"
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/db_xref="taxon:3880"
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Pred. No. 6.8e-38;
0; Mismatches 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Ewylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., E., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public, Soybean, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
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                                        167
                             /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: 1-vodkin@uiuc.edu"
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                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
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                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DH10B"
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV428823 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM073a12_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                             Contact: Erika Asamizu
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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DNA Res. 7 (2), 127-130
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                                                                                                                                                                                                                                           asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
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/dev_stage="young plants (two-week old)"
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        XhoI;
                                                                                                      /organism="Lotus japonicus"
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/clone="MWM073a12_r"
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                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Public, Soybean, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE020246 483 bp mRNA EST 06-JUN-2000 sm42d08.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-6568 5' similar to TR:P93330 P93330 MTN13 GENE. ;, mRNA
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sy
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max
                                                                           Email: est@watson.wustl.edu
                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                         Public Soybean EST Project
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High quality sequence stop: 420.
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                                                                                              column. The column eluent was then ligated into Stratagene's pBluescript II xR Predigested vector (pBluescript II sK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The xhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"vector: pBluescript II XR; Site_1: EcoRI; Site_2: Xho1; The mRNA was isolated from rocks of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed to the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesize the cDNA. First-strand synthesis was with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glycine max"
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/clone="GENOME SYSTEMS CLONE ID:
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/lab_host="DH10B"
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Query Match 361 241 196 181 136 121 Local Similarity 60.8 tes 288; Conservative 76 61 16 1 ggtgtgtttaattatgagactgagaccacctctgttatcccagcagctcgactgttcaag cacaccaaaggtgaccatgaggtgaaggcaggcaggttaaggcaagtaaagaaatgggc tacaattacagcgtgatcgagggcggtcccataggcgacacattggagaagatctccaac gttgaaaacattgaaggaaatggagggcctggaaccattaagaagatcagctttcccgaa 180 GGTGTTTTCACTTCTGAAAGCGAACACGTTTCCCCCCGTCTCTGCTGCAAAATTATACAAA 75 TACAACTATAGTGTGATTGAAGGCAGTGCATTGTCGGAGCCATTGGAGAAGATATGTTAT GG-----TTTAGGTTATGTGAAGCACCACGTAGATGCAATTGACACAGAAAACTATGTG ggcctccctttcaagtacgtgaaggacagagttgatgaggtggaccacacaaacttcaaa GTAGAAACCATTGAAGGAGGATGGAGGGCCAGGAACCATTAAGAAGCTTACTCTTGCTGAA GCTATTGTCCTAGATGCCAGCAATGTCTTCCCAAAAGCATTGCCAAATTTCATTAAGAGC gcctttatccttgatggcgataacctctttccaaaaggttgcaccccaagccattagcagt 120 34.2%; 60.8%; 0; Score 164; DB 32; Pred. No. 1.2e-37; 0; Mismatches 180; Length 483; Indels 6; 420 135 300 249 240 195 ۲,

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Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson wustl.edu

Email: estewatson wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 Foor further information

call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

Insert Length: 940 Std Error: 0.00
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW234941 498 bp mRNA EST 17-JUL-2000 sf21a03.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-581 5' similar to SW:SAM2_SOYBN P26987 STRESS-INDUCED
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                                                                                                                                                                                         /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDAilO priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After
cloned pfu DNA polymerase. ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation
                                                                                                                                                                       second-strand synthesis, the cDNA ends were filled in with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
/clone="CENOME SYSTEMS CLONE ID: Gm-c1028-581"
/clone_lib="Gm-c1028"
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  Shoemaker R/Public Soybean EST Project
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287; Conser
                                                     A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurl, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1988606 507 bp mRNA EST 17-JUL-2000 sd05a12.yl Gm-c1020 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1020-791 5' similar to SW:SAM2_SOYBN P26987 STRESS-INDUCED
Public Soybean EST Project Unpublished (1999)
                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
                                                                                                                                                                                                                                                                                                                                                                Glycine max
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SAM22. ; , mRNA sequence.
                                                                                                                                                                                                                                         (bases 1 to 507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:5820400
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241 tacaattacagcgtgatcgagggcggtcccataggcgacacattggagaagatctccaac 300
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                                                                       214 GATGGAGAAACCAAGTTTGTGCTGCACAAAATAGAAAGCATTGATGAGGCGAACTTGGGA 273
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                                                                                                                                                                                                                                                                                                                                                                              61 gcctttatccttgatggcgataacctctttccaaaggtttgcaccccaagccattagcagt 120
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                                                                                                                     gttgaaaacattgaaggaaatggagggcctggaaccattaagaagatcagctttcccgaa 180
                                                                                                                                                                                                                                                                                                                                              GCCCTAGTTACAGATGCCGACAACGTCATCCCAAAGGCT---CTTGATTCCTTCAAGAGT
                                                                                                                                                                                                       GTTGAAAACGTTGAGGGAAATGGTGGCCCCAGGAACCATCAAGAAGATCACTTTCCTTGAG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; This cDNA library was constructed from mRNA isolated from nodules on the roots of 2.5 month-old Glycine max 'Williams' plants that were greenhouse grown. The The cDNA library was prepared using the Stratagene pBluescript II SK(+) library construction kit. First strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nuclectide (v=A, C, or G) was added to the 3' end of the primer [GARGAGAGAGAGAGAGACACACTGCTGCAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size- fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from Pharmacia. The column eluent was ligated to EcoRI adaptors and phosphporylated. The XhoI sites in the cDNA would be profected by their hemimethylated estatus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protected by their hemimethylated status. The CDNA constructs were size- fractionated with a 500 bp cutoff, using GibcobRL Life Technologies' CDNA Size Predigested vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with CDNA inserts, based on size (n-56) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence (n=16). This library was constructed by Dr. Paul
Keim and Dr. Virginia Coryell."
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/clone_lib="Gm-c1020"
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pred. No. 1.6e-37;
0; Mismatches 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCCAAATTGGTTGCTGGTCCCAATGGAGGGTCTGCTGGGAAGCTCACTGTCAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagataaagatagtggcaacccctgatggaggatccatcttgaagatcagcaacaagtac 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAGCTACAGCGTGGTTGGGGGGTGCTGCATTGCCAGACACGGCGGAGAAGATCACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,D., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert Length: 812 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St.
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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314 286 1810
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                                                                                                Anote-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from 'Desloy 5710' seedling roots. Tissue was taken from 7-day-old seedlings that had been propagated on paper towels with distilled water. Tissue was taken from the tipt to the first lateral root, usually about 3cm from the tip, and flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 20040) was used to
                       synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor
                                                                                                                                                                                                                                                                                                                                   /tissue_type="'Desloy 5710' seedling roots"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                             /clone="GENOME SYSTEMS CLONE ID: Gm-c1033-1068"
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Query Match 34.1%;
Best Local Similarity 60.5%;
Matches 287; Conservative
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                                                                           cacaccaaaggtgaccatgaggtgaaggcaggagcaggttaaggcaagtaaagaaatgggc 420
                                                                                                                                       gagataaagatagtggcaacccctgatggaggatccatcttgaagatcagcaacaagtac 360
                                                                                                                                                                                                 tacaattacagcgtgatcgagggcggtcccataggcgacacattggagaagatctccaac 300
                                                                                                                                                                                                                                          GATGGAGAAAGCAAGTTTGTGTTGCACAAAATAGAATCAGTTGACGAGGCAAACTTGGGA 287
                                                                                                                                                                                                                                                                                                     GCTCTAGTTACAGATGCCGACAACGTCATCCCAAAGGCTGT---CGAAGCCTTCAGGAGT 167
                                                                                                                                                                                                                                                                                                                                                                                  gcctttatccttgatggcgataacctctttccaaaggttgcaccccaagccattagcagt 120
                                                             CAAACCAAAGGAGATGCTCAGCCCAACCCAGACGACGTCAAAATTGGCAAAGTCAAGTCT
                                                                                                                       GAATGCAAATTGGCTGCTGGCGCCAACGGAGGGTCTGCTGGGAAGCTAACTGTCAAATAC 407
                                                                                                                                                                                TACAGCTATAGCGTAGTTGGTGGAGTTGGGTTGCCAGACACAGTGGAGAAGATCACATTC 347
                                                                                                                                                                                                                                                             ggcctccctttcaagtacgtgaaggacagagttgatgaggtggaccacacaaacttcaaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152
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